

FIG. 1

USE OF ANTIBODIES AGAINST THE MUC18 ANTIGEN

Bar-Eli, et al.

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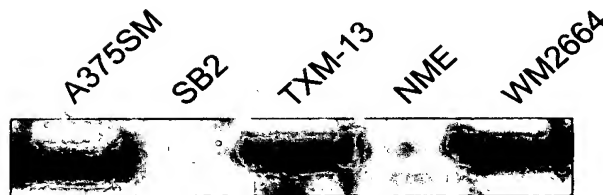


FIG. 2

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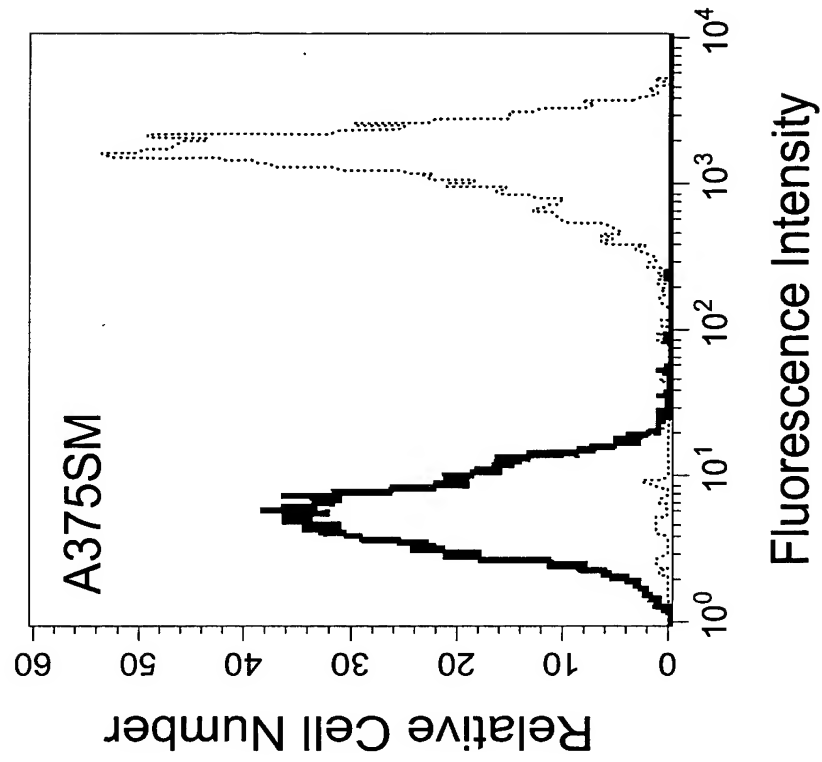


FIG. 3B

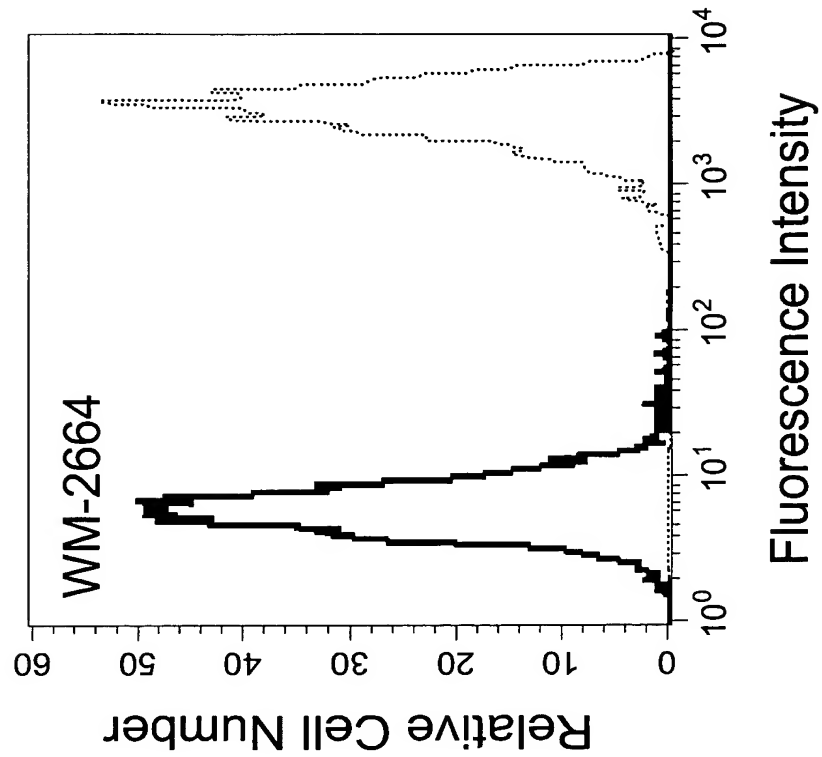


FIG. 3A

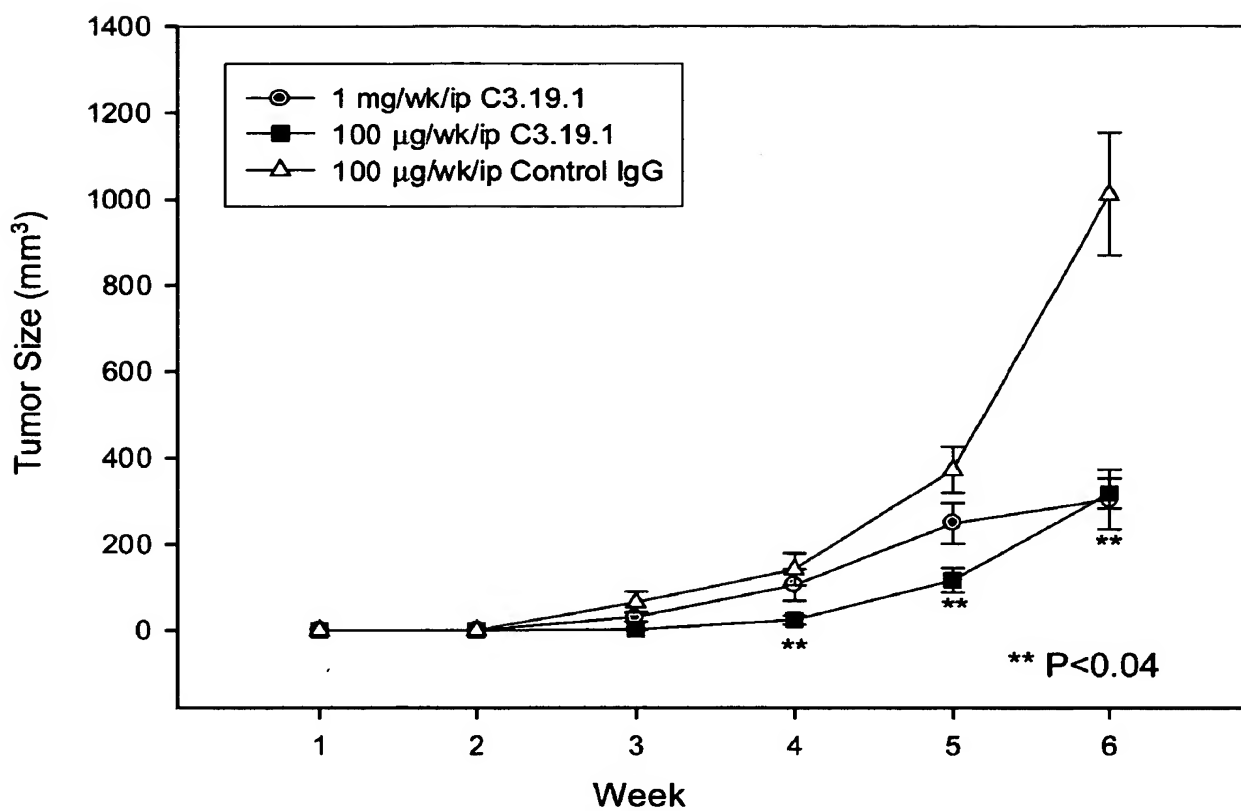


FIG. 4

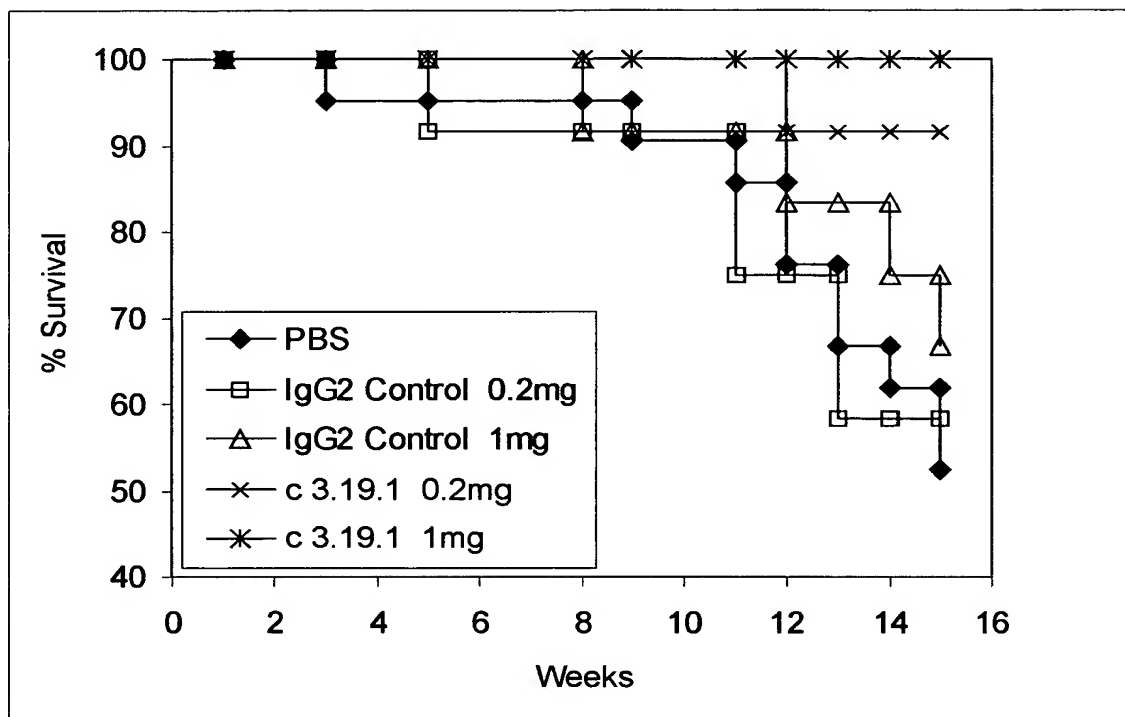


FIG. 5

ANTI-MUC18 ANTIBODY C3.19.1

Nucleotide Sequence of Heavy Chain Variable Region

5' -

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC
ACTGTCTCTGGTGGCTCCATCAGTAGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGA
CTGGAGTGGATTGGCTATATCTATTACACTTGGACCTCCAACCTACAACCCCTCCCTCAAGAGTCGC
GTCACCATATCAGTGGACACGTCCAAAAACCAGTTCTCCCTGAGGCTGAGTTCTGTGACCGCTGCG
GACACGGCCGTTTATTACTGTGCGAGAGATCAGGGGCAGTGGTTACTACCCGATGCTTTTGATATC
TGGGGCCAAGGGACAATGGTCACCGTCTCTTCAG 3' (SEQ ID NO: 3)

Amino Acid Sequence of Heavy Chain Variable Region

QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYPNPSLKSR
VTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWQGQTMVTVSS (SEQ ID NO:1)

Nucleotide Sequence of Light Chain Variable Region

5' -

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCC
TGCAGGTCTAGTCAGAGCCTCCTGCGTAGTAATGGATACAACCTATTTGGATTGGTACCTGCAGAAG
CCAGGACAGTCTCCACATCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGG
TTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTT
GGGGTTTATTACTGCATGCAAGCTCAACAAAGTCCGATCACCTTCGGCCAAGGGACACGACTGGAG
ATTAAAC 3' (SEQ ID NO: 4)

Amino Acid Sequence of Light Chain Variable Region

DIVMTQSPLSLPVTPGEPASISCRSSQSLLRNNGYNYLDWYLQKPGQSPHLLIYLGSNRASGVPDR
FSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGRLEIK (SEQ ID NO: 2)

FIG. 6

ANTI-MUC18 ANTIBODY C6.11.13

Nucleotide Sequence of Heavy Chain Variable Region

5' -

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
ACTGTCTCTGGTGGCTCCATCAGCAGTGGTACTTACCACTGGAGCTGGATCCGCCAGCACCCAGGG
AAGGGCCTGGAGTGGATTGGGTACATCTATTACAGTGGGAGCACCTACTACAACCCGTCCCTCAAG
AGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACT
GCCGCGGACACGGCCGTGTATTACTGTGCGAGAGGGGGAGATGGCTACAAGTACTGGGGCCAGGGA
ACCCTGGTCACCGTCTCCTCAG-3' (SEQ ID NO: 7)

Amino Acid Sequence of Heavy Chain Variable Region

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYKYWGQGLTVTVSS (SEQ ID NO: 5)

Nucleotide Sequence of Light Chain Variable Region

5'

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC
TGCAGGGCCAGTCAGAGTGTTAGCAACAACCTTAGCCTGGTATCAGCAGAAACCTGGCCAGGCTCCC
AGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCACTGGCAGTGGG
TCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGT
CAGCAGTATAATAACTGGCCTCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAAC 3'
(SEQ ID NO: 8)

Amino Acid Sequence of Light Chain Variable Region

EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSG
SGTEFTLTISSLQSEDFAVYYCQQYNWPRTFGQGTKVEIK (SEQ ID NO: 6)

FIG. 7

ANTI-MUC18 ANTIBODY C3.10

Nucleotide Sequence of Heavy Chain Variable Region

```
1 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC CCTGTCCCTC
61 ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT GGAGCTGGAT CCGGCAGCCC
121 CCAGGGAAGG GACTGGAGTG GATTGGCTAT ATCTATTACA CTTGGACCAC CAACTACAAC
181 CCCTCCCTCA AGAGTCGCGT CACCATATCA GTGGACACGT CCAAGAACCA GTTCTCCCTG
241 AGGCTGAGCT CTGTGACCGC TGC GGACACG GCCCTTTATT ACTGTGCGAG AGATCAGGGG
301 CAGTGGTTAC TACCCGATGC TTTTGATATC TGGGGCCAAG GGACAATGGT CACCGTCTCT
361 TCAG (SEQ ID NO: 11)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
1 QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYYSWIRQP PGKGLEWIGY IYYTWTNRYN
61 PSLKSRVTIS VDTSKNQFSL RLSSVTAADT ALYYCARDQG QWLLPDAFDI WQGQTMVTVS
121 S (SEQ ID NO: 9)
```

Nucleotide Sequence of Light Chain Variable Region

```
1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
61 ATCACTTGCC GGGCAAGTCA GAGCATTAGC AACTATTTAA ATTGGTATCA GCAGAAACCA
121 GGAAAAGCCC CTAAGCTCCT GATCTATGGT GCATCCAGTT TGCAAAGTGG GGTCCCATCA
181 AGGTTCAAGT GCAGTGGATC TGGGACAGAT TTTACTCTCA CCATCAGCAG TCTGCAACCT
241 GAAGATTTTG CAACCTACTA CTGTCGACAG AGTTACAGTA CCCCTCCGGA GTGCAGTTTT
301 GGCCAGGGGA CCAAGCTGGA GATCAAAC (SEQ ID NO: 12)
```

Amino Acid Sequence of Light Chain Variable Region

```
1 DIQMTQSPSS LSASVGDRVT ITCRASQSIG NYLNWYQQKP GKAPKLLIYG ASSLQSGVPS
61 RFSGSGSGTD FTLTISSLQP EDFATYYCRQ SYSTPPECSF GQGTKLEIK (SEQ ID NO:10)
```

FIG. 8

ANTI-MUC18 ANTIBODY C3.22

Nucleotide Sequence of Heavy Chain Variable Region

```
1 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCACAGAC CCTGTCCCTC
61 ACCTGCACTG TCTCTGGTGG CTCCATCAGC AGTGGTGGTT ACTACTGGAC TTGGATCCGC
121 CAGCACCCAG GGAAGGGCCT GGAGTGGATT GGGTTCATCT ATTACAGTGG GAGCACCTAC
181 TACAACCCGT CCCTCAAGAG TCGAGTTACC ATATCAGTAG ACACGTCTAA GAACCAGTTC
241 TCCCTGAAGC TGAGCTCTGT GACTGCCGCG GACACGGCCG TGTATTACTG TGCAGAGAGAG
301 GGAGATGGCT TTGACTACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCCTC AG
(SEQ ID NO: 15)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
1 QVQLQESGPG LVKPSQTLST TCTVSGGSIS SGGYYWTWIR QHPKGLEWI GFIIYSGSTY
61 YNPSLKSRVT ISVDTSKNQF SLKLSSVTAA DTAVYYCARE GDGFDYWGQG TLVTVSS
(SEQ ID NO: 13)
```

Nucleotide Sequence of Light Chain Variable Region

```
1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
61 ATCACTTGCC GGGCAAGTCA GGGCATTAGA AATGATTTAG GCTGGTATCA GCAGAAACCA
121 GGGAAAGCCC CTAAGCGCCT GATCTATGCT GCATCCAGTT TGCAAAGTGG GGTCCCATCA
181 AGGTTCAGCG GCAGTGGATC TGGGACAGAA TTTACTCTCA CAATCAGCAG CCTGCAGCCT
241 GAAGATTTTG CAACTTATTA CTGTCTACAG CATAATAGTT ACCCGCTCAC TTTCGGCGGA
301 GGGACCAAGG TGGAGATCAA AC (SEQ ID NO: 16)
```

Amino Acid Sequence of Light Chain Variable Region

```
1 DIQMTQSPSS LSASVGDRVT ITCRASQGIR NDLGWYQQKP GKAPKRLIYA ASSLQSGVPS
61 RFSGSGSGTE FTLTISSLQP EDFATYYCLQ HNSYPLTFGG GTKVEIK (SEQ ID NO: 14)
```

FIG. 9

ANTI-MUC18 ANTIBODY C3.27

Nucleotide Sequence of Heavy Chain Variable Region

```
1 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC CCTGTCCCTC
61 ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT GGAGCTGGAT CCGGCAGCCC
121 CCAGGGAAGG GACTGGAGTG GATTGGCTAT ATCTATTACA CTTGGACCTC CAACTACAAC
181 CCCTCCCTCA AGAGTCGCGT CACCATATCA GTGGACACGT CCAAGAACCA GTTCTCCCTG
241 AGGCTGAGTT CTGTGACCGC TGGGACACG GCCGTTTACT ACTGTGCGAG AGATCAGGGG
301 CAGTGGTTAC TACCCGATGC TTTTGATATC TGGGGCCAAG GGACAATGGT CACCGTCTCT
361 TCAG (SEQ ID NO: 19)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
1 QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYVSWIRQP PGKGLEWIGY IYYTWSNRYN
61 PSLKSRVTIS VDTSKNQFSL RLSSVTAADT AVYYCARDQG QWLLPDAFDI WGQGTMTVTS
121 S (SEQ ID NO: 17)
```

Nucleotide Sequence of Light Chain Variable Region

```
1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
61 ATCACTTGCC GGGCAAGTCA GGGCATTAGA AATGATTTAG GCTGGTATCA GCAGAAACCA
121 GGGAAAGCCC CTAAGCGCCT GATCTATGCT GCATCCAGTT TGCAAAGTGG GGTCCCATCA
181 AGGTTCAGCG GCAGTGGATC TGGGACAGAG TTTACTCTCA CAATCAGCAG CCTGCAGCCT
241 GAAGATTTTG CAACTTATTA CTGTCTACAG CATAATAGTT ACCCGTGGAC GTTCGGCCAA
301 GGGACCAAGG TGGAAATCAA AC (SEQ ID NO: 20)
```

Amino Acid Sequence of Light Chain Variable Region

```
1 DIQMTQSPSS LSASVGDRVT ITCRASQGIR NDLGWYQQKP GKAPKRLIYA ASSLQSGVPS
61 RFSGSGSGTE FTLTISSLQP EDFATYYCLQ HNSYPWTFGQ GTKVEIK
(SEQ ID NO: 18)
```

FIG. 10

ANTI-MUC18 ANTIBODY C3.45

Nucleotide Sequence of Heavy Chain Variable Region

```

1 CAGGTTTCAGC TGGTGCAAGC GGGAGCTGAG GTGAAGAAGC CTGGGGCCTC AGTGAAGGTC
61 TCCTGCAAGG CTTCTGGTTA CACCTTTTTT AGCTATGGTT TCAGCTGGGT GCGACAGGCC
121 CCTGGACAAG GGCTTGAGTG GCTGGGATGG ATCAGCGCTT ACAATGGTAA CACAACTAT
181 GCACAGAAGC TCCAGGGCAG AGTCACCATG ACCACAGACA CTTCCACGAG CACAGCCTAC
241 ATGGAGCTGA GGAGCCTGAG ATCTGACGAC ACGGCCGTGT ATTACTGTGC GAGAGAACT
301 AAGGTTTCGGG GAGTCCACTA CTACGGTATG GACGTCTGGG GCCAAGGGAC CACGGTCACC
361 GTCTCCTCAG (SEQ ID NO: 23)

```

Amino Acid Sequence of Heavy Chain Variable Region

```

1 QVQLVQSGAE VKKPGASVKV SCKASGYTFF SYGFSWVRQA PGQGLEWLGW ISAYNGNTNY
61 AQKLQGRVTM TTDSTSTAY MELRSLRSD TAVYYCARET KVRGVHYYGM DVWGQGTIVT
121 VSS (SEQ ID NO: 21)

```

Nucleotide Sequence of Light Chain Variable Region

```

1 DIVMTQSPDS LAVSLGERAT IICKSSQSIL YSSNNKNYLG WYQQKPGQPP KLLIYWASTR
61 ESGVPARFSG SGSGTDFTLT INSLOAEDVA VYYCQQYYST PRSFGQGTMV EIK (SEQ ID
NO: 24)

```

Amino Acid Sequence of Light Chain Variable Region

```

1 GACATCGTGA TGACCCAGTC TCCAGACTCC CTGGCTGTGT CTCTGGGCGA GAGGGCCACC
61 ATCATCTGCA AGTCCAGCCA GAGTATTTTA TACAGCTCCA ACAATAAGAA CTA CT TAGGT
121 TGGTACCAGC AGAAACCAGG ACAGCCTCCT AAGCTGCTCA TTTACTGGGC ATCTACCCGG
181 GAATCCGGGG TCCCTGCCCC ATTCAGTGGC AGCGGGTCTG GGACAGATTT CACTCTCACC
241 ATCAACAGCC TGCAGGCTGA AGATGTGGCA GTTTATTACT GTCAGCAATA TTATAGTACT
301 CCTCGGTCGT TCGGCCAAGG GACCATGGTG GAAATCAAAC (SEQ ID NO 22)

```

FIG. 11

ANTI-MUC18 ANTIBODY C3.65

Nucleotide Sequence of Heavy Chain Variable Region

```

1  CAGGTGCAGC  TGCAGGAGTC  GGGCCCAGGA  CTGGTGAAGC  CTTACAGAC  CCTGTCCCTC
61  ACCTGCACTG  TCTCTGGTGG  CTCCATCAAC  AGTGGTGGTT  GCTACTGGAG  CTGGATCCGC
121 CAGCACCCAG  GGAAGGGCCT  GGAGTGGATT  GGGTACATCT  ATTCCAGTGG  GAGCACCTAC
181 TACAACCCGT  CCCTCAAGAG  TCGAATTACC  TTATCAGTAG  ACACGTCTAA  GAACCAGTTC
241 TCCCTGAAGC  TGAAGTCTAT  GACTGCCGCG  GACACGGCCG  TGTATTACTG  TCGGAGAGAT
301 CGGGAAACAG  CTGGTTTGA  CTAAGTGGGC  CAGGGAACCC  TGGTCACCGT  CTCCTCAG
(SEQ ID NO: 27)

```

Amino Acid Sequence of Heavy Chain Variable Region

```

1  QVQLQESGPG  LVKPSQTLST  TCTVSGGSIN  SGGCYWSWIR  QHPGKGLEWI  GYIYSSGSTY
61  YNPSLKSRIT  LSVDTSKNQF  SLKLNSMTAA  DTAIVYCARD  RETAGFDYWG  QGTLVTVSS
(SEQ ID NO: 25)

```

Nucleotide Sequence of Light Chain Variable Region

```

1  GACATCCAGA  TGACCCAGTC  TCCATCCTCC  CTGTCTGCAT  CTGTAGGAGA  CAGAGTCACC
61  ATCACTTGCC  AGGCGAGTCA  GGACATTAAC  AACTATTTAA  ATTGGTATCA  GCAGAAACCA
121 GGGAAAGCCC  CTAAGCTCCT  GATCTACGAT  GCATCCAATT  TGGAAACAGG  GGTCCCATCA
181 AGGTTCAGTG  GAAGTGGATC  TGGGACAGAT  TTTACTTTCA  CCATCAGCGG  CCTGCAGCCT
241 GAGGATATTG  CAACATATTA  CTGTCAACAG  TATGATACTC  TCCCTCTCAC  TTTCGGCGGC
301 GGGACCAAGG  TGGAGATCAA  AC (SEQ ID NO: 28)

```

Amino Acid Sequence of Light Chain Variable Region

```

1  DIQMTQSPSS  LSASVGDRVT  ITCQASQDIN  NYLNWYQQKP  GKAPKLLIYD  ASNLETGVPS
61  RFSGSGSGTD  FTFTISGLQP  EDIATYYCQQ  YDTLPLTFGG  GTKVEIK (SEQ ID NO: 26)

```

FIG. 12

ANTI-MUC18 ANTIBODY C6.1

Nucleotide Sequence of Heavy Chain Variable Region

```
1 CAGGTGCAGC TGGTGGAGTC GGGGGGAGGC GTGGTCCAGC CTGGGAGGTC CCTGAGACTC
61 TCCTGTGCAG CCTCTGGATT CACCTTCAGT AGCTATGCCA TGCACTGGGT CCGCCAGGCT
121 CCAGGCAAGG GGCTGGAGTG GGTGGCAGTT ATATCATATG ATGGAAGTAA TAAATACTAT
181 GCAGACTCCG TGAAGGGCCG ATTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT
241 CTGCAAATGA ACAGCCTGAG AGCTGAGGAC ACGGCTGTGT ATTACTGTGC GAGATCGATT
301 TTTGGAGTGG TTATCGACTA CGGTATGGAC GTCTGGGGCC AAGGGACCAC GGTCACCGTC
361 TCCTCAG (SEQ ID NO: 31)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
1 QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYAMHWVRQA PGKGLEWVAV ISYDGSNKYY
61 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARSI FGVVIDYGMD VWGQGTTVT
121 SS (SEQ ID NO: 29)
```

Nucleotide Sequence of Light Chain Variable Region

```
1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
61 ATCACTTGCC GGGCGAGTCA GGGCATTAGA AATTATTTAG CCTGGTATCA GCAGAATCCA
121 GGGAAAGTTC CTAAGCTCCT GATCTATGGT GCATCCACTT TGCAATCAGG GGTCCCATCT
181 CGGTTCAGTG GCAGTGGATC TGGGACAGAT TTTACTCTCA CCATCAGCAG CCTGCAGCCT
241 GAAGATGTTG CAACTTATTA CTGTCAAAG TTTAGCAGTC CCCCATTCAC TTTCGGCCCT
301 GGGACCAAAG TGGATATCAG TC (SEQ ID NO: 32)
```

Amino Acid Sequence of Light Chain Variable Region

```
1 DIQMTQSPSS LSASVGDRVT ITCRASQGIR NYLAWYQQNP GKVPKLLIYG ASTLQSGVPS
61 RFSGSGSGTD FTLTISSLQP EDVATYYCQK FSSPPFTFGP GTKVDIS (SEQ ID NO: 30)
```

FIG. 13

ANTI-MUC18 ANTIBODY C6.9

Nucleotide Sequence of Heavy Chain Variable Region

```
1 CAGGTGCAGC TGGAGCAGTC GGGGCCAGGA CTGGTGAAGC CTTCAGAGAC CCTGTCCCTC
61 ACCTGCACTG TCTCTGGTGG CTCCATCAGC AGTGGTACTT ACCACTGGAG CTGGATCCGC
121 CAGCACCCAG GGAGGGGCCT GGAGTGGATT GGATACATCT ATTACAGTGG GAGCACCTAC
181 CACAACCCGT CCCTCAAGAG TCGAATTACC ATATCAGTAG ACACGTCTAA GAACCAGTTC
241 TCCCTGAAGC TGAGCTCTGT GACGGCCGCG GACACGGCCG TGTATTACTG TGCGAGAGGG
301 GGAGATGGCT ACAGATACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCCTC AG
(SEQ ID NO: 35)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
1 QVQLEQSGPG LVKPSETLSL TCTVSGGSIS SGTYHWSWIR QHPGRGLEWI GYIYYSGSTY
61 HNP SLKSRIT ISVDTSKNQF SLKLSSVTAA DTA VYYCARG GDGYRYWGQG TLVTVSS
(SEQ ID NO: 33)
```

Nucleotide Sequence of Light Chain Variable Region

```
1 GAAATAGTGA TGACGCAGTC TCCAGCCACC CTGTCTGTGT CTCCAGGGGA AAGAGCCACC
61 CTCTCCTGCA GGGCCAGTCA GAGTATTAGC AACAACTTCG CCTGGTACCA GCAGAAACCT
121 GGCCAGGCTC CCAGGCTCCT CATCTTTGGT GCATCCACCA GGGCCACTGG TATCCCAGCC
181 AGGTTCAGTG GCAGTGGGTC TGGGACAGAA TTCACTCTCA CCATCAGCAG CCTACAGTCT
241 GAAGATTTTG CAGTTTATTA CTGTCAGCAG TATAATAACT GGCCTCGGAC GTTCGGCCAA
301 GGGACCAAGG TGGAAATCAA AC (SEQ ID NO: 36)
```

Amino Acid Sequence of Light Chain Variable Region

```
1 EIVMTQSPAT LSVSPGERAT LSCRASQSIG NFAWYQQKP GQAPRLLIFG ASTRATGIPA
61 RFSGSGSGTE FTLTISLQS EDFAVYYCQQ YNNWPRTFGQ GTKVEIK (SEQ ID NO: 34)
```

FIG. 14

ANTI-MUC18 ANTIBODY C6.2

Nucleotide Sequence of Heavy Chain Variable Region

```

1  CAGGTGCAGC  TGCAGGAGTC  GGGCCCAGGA  CTGGTGAAGC  CCTCGGAGAC  CCTGTCCCTC
61  ACCTGCACTG  TCTCTGGTGG  CTCCATCAGT  ACTTACTACT  GGAGTTGGAT  CCGGCAGCCC
121  CCAGGGAAGG  GACTGGAGTG  GATTGGATAC  ATCTATTACA  CTGGGAACAC  CTAACAAC
181  CCCTCCCTCA  AGAGTCGAGT  CACCGTTTCA  GTTGACACGT  CCAAGAACCA  GTTCTCCCTG
241  AAGCTGAAGT  CTGTGACCGC  TGCAGGACAG  GCCGTGTATT  ACTGTGCGAG  AGATCCAGGC
301  CAGTGGCTGG  TCCCTGATGC  TTTTGATATC  TGGGGCCAAG  GGACAATGGT  CTCCGTCTCT
361  TCAG  (SEQ ID NO: 39)

```

Amino Acid Sequence of Heavy Chain Variable Region

```

1  QVQLQESGPG  LVKPSETLSL  TCTVSGGSIS  TYYWSWIRQP  PGKGLEWIGY  IYYTGNTYYN
61  PSLKSRVTVS  VDTSKNQFSL  KLSNVTAADT  AVYYCARDPG  QWLVPDAFDI  WGQGTMTSVS
121  S  (SEQ ID NO: 37)

```

Nucleotide Sequence of Light Chain Variable Region

```

1  GATATTGTGA  TGAATCAGTC  TCACTCTCC  CTGCCCCTCA  TTCCTGGAGA  GCCGGCCTCC
61  ATCTCCTGCA  GGTCTAGTCA  GAGCCTCCTG  CAGAGTAATG  GAAACAATA  TTTGGATTGG
121  TACCTGCAGA  AGCCAGGGCA  GTCTCCACAG  CTCCTGATCT  ATTTGGGTTC  TAATCGGGCC
181  TCCGGGGTCC  CTGACAGGTT  CAGTGGCAGT  GGATCAGGCA  CAGATTTTAC  ACTGAAAATC
241  AGCAGAGTGG  AGGCTGACGA  TGTGTTGGAT  TATTACTGCA  TGCAAGCTCT  CCAAATTCCT
301  CTCACCTTTCG  GCGGAGGGAC  CAAGGTGGAG  ATCAAAC  (SEQ ID NO: 40)

```

Amino Acid Sequence of Light Chain Variable Region

```

1  DIVMTQSPLS  LPVIPGEPAS  ISCRSSQSLL  QSNNGNNYLDW  YLQKPGQSPQ  LLIYLGSNRA
61  SGVPDRFSGS  GSGTDFTLKI  SRVEADDVGI  YYCMQALQIP  LTFGGGTKVE  IK
(SEQ ID NO: 38)

```

FIG. 15

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Section 1						
	(1)	10	20	30	40	53
A15-3.10_HC	(1)	QVQLQESGPGLVKPS	ETLSLTCTVSGGSI	SSYYWSWIRQPPGK	GLEWIGYIYY	
VH4-59	(1)	QVQLQESGPGLVKPS	ETLSLTCTVSGGSI	SSYYWSWIRQPPGK	GLEWIGYIYY	
Consensus	(1)	QVQLQESGPGLVKPS	ETLSLTCTVSGGSI	SSYYWSWIRQPPGK	GLEWIGYIYY	
Section 2						
	(54)	54	60	70	80	90
A15-3.10_HC	(54)	EWITNYNPSLKSRVT	ISVDTSKNQFSLRL	SSVTAADTANNYCAR	DQGQWLLPD	
VH4-59	(54)	SGSTINYNPSLKSRVT	ISVDTSKNQFSLRL	SSVTAADTANNYCAR	-----	
Consensus	(54)	S STINYNPSLKSRVT	ISVDTSKNQFSLKL	SSVTAADTALYYCAR		
Section 3						
	(107)	107	121			
A15-3.10_HC	(107)	AFDIWGQGTMTVSS				
VH4-59	(98)	-----				
Consensus	(107)					

positives: 79.3%	identity: 76.0%
------------------	-----------------

FIG. 16

		Section 1						
	(1)	1	10	20	30	40	53	
A15-3.10_LC	(1)	DIQMTQSPSSLSASVGDRTITTCRASQISINYNWYQQKPGKAPKLLIYSAAS						
O2	(1)	DIQMTQSPSSLSASVGDRTITTCRASQISINYNWYQQKPGKAPKLLIYSAAS						
Consensus	(1)	DIQMTQSPSSLSASVGDRTITTCRASQISINYNWYQQKPGKAPKLLIYSAAS						
		Section 2						
	(54)	54	60	70	80	90	106	
A15-3.10_LC	(54)	LQSGVPSRFSGSGGTDFLTITISSLQPEDFATYYCRRSYSTPPECSFGQGTKL						
O2	(54)	LQSGVPSRFSGSGGTDFLTITISSLQPEDFATYYCRRSYSTPPECSFGQGTKL						
Consensus	(54)	LQSGVPSRFSGSGGTDFLTITISSLQPEDFATYYCRRSYSTPPECSFGQGTKL						
		Section 3						
	(107)	107						
A15-3.10_LC	(107)	EIK						
O2	(96)	---						
Consensus	(107)							

positives: 85.3%	identity: 84.4%
------------------	-----------------

FIG. 17

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Section 1									
	1	10	20	30	40	53			
A15-3.22_HC	(1)	QVQLQESGPGLVKPSQ	TL	SL	TCTV	SSGGYS	SSGGYS	SSGGYS	SSGGYS
VH4-31	(1)	QVQLQESGPGLVKPSQ	TL	SL	TCTV	SSGGYS	SSGGYS	SSGGYS	SSGGYS
Consensus	(1)	QVQLQESGPGLVKPSQ	TL	SL	TCTV	SSGGYS	SSGGYS	SSGGYS	SSGGYS
Section 2									
	54	60	70	80	90	106			
A15-3.22_HC	(54)	YYSGSTYYNPSLKSRVT	IS	VD	TSKNQF	SLKLS	SSVT	AADT	AVYYCAR
VH4-31	(54)	YYSGSTYYNPSLKSRVT	IS	VD	TSKNQF	SLKLS	SSVT	AADT	AVYYCAR
Consensus	(54)	YYSGSTYYNPSLKSRVT	IS	VD	TSKNQF	SLKLS	SSVT	AADT	AVYYCAR
Section 3									
	107	117							
A15-3.22_HC	(107)	WGQGT	LV	TV	SS				
VH4-31	(100)	-----							
Consensus	(107)	-----							

positives: 84.6%	identity: 82.9%
------------------	-----------------

FIG. 18

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Section 1							
	(1)	1	10	20	30	40	53
A15-3.22_LC	(1)	DIQMTQSPSSLSASVGDRVTITTCRASQGI RNDLGWYQQKPGKAPKRLIYAASS					
A30	(1)	DIQMTQSPSSLSASVGDRVTITTCRASQGI RNDLGWYQQKPGKAPKRLIYAASS					
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITTCRASQGI RNDLGWYQQKPGKAPKRLIYAASS					
Section 2							
	(54)	54	60	70	80	90	106
A15-3.22_LC	(54)	LQSGVPSRFSGSGGTEFTLTISSLQPEDE FATTYICLQHNSYP					
A30	(54)	LQSGVPSRFSGSGGTEFTLTISSLQPEDE FATTYICLQHNSYP					
Consensus	(54)	LQSGVPSRFSGSGGTEFTLTISSLQPEDE FATTYICLQHNSYP					
Section 3							
	(107)	107					
A15-3.22_LC	(107)	K					
A30	(96)	-					
Consensus	(107)						

positives: 88.8% identity: 88.8%

FIG. 19

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Section 1						
	(1)	10	20	30	40	53
A15-3.27_HC	(1)	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY				
VH4-59	(1)	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY				
Consensus	(1)	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY				
Section 2						
	(54)	60	70	80	90	106
A15-3.27_HC	(54)	TWTSNYPNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR				
VH4-59	(54)	SGSTNYPNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR				
Consensus	(54)	SSNYPNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR				
Section 3						
	(107)	121				
A15-3.27_HC	(107)	AFDIWGQGTMTVSS				
VH4-59	(98)	-----				
Consensus	(107)					

positives: 79.3%	identity: 76.0%
------------------	-----------------

FIG. 20

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Section 1									
	1	10	20	30	40	53			
(1)	(1)								
A15-3.27_LC	(1)	DIQMTQSPSSL	SASVGD	RVTIT	TCRASQ	GIRNDL	GWYQQ	KPGKAP	KRLIYAASS
A30	(1)	DIQMTQSPSSL	SASVGD	RVTIT	TCRASQ	GIRNDL	GWYQQ	KPGKAP	KRLIYAASS
Consensus	(1)	DIQMTQSPSSL	SASVGD	RVTIT	TCRASQ	GIRNDL	GWYQQ	KPGKAP	KRLIYAASS
Section 2									
	54	60	70	80	90	106			
(54)	(54)								
A15-3.27_LC	(54)	LQSGVPS	RFSGSG	GTEFTL	TIS	SLQPE	DFATY	YCLQHN	SYPWTFGQGTKVEI
A30	(54)	LQSGVPS	RFSGSG	GTEFTL	TIS	SLQPE	DFATY	YCLQHN	SYPWTFGQGTKVEI
Consensus	(54)	LQSGVPS	RFSGSG	GTEFTL	TIS	SLQPE	DFATY	YCLQHN	SYPWTFGQGTKVEI
Section 3									
(107)	(107)								
A15-3.27_LC	(107)	K							
A30	(96)	-							
Consensus	(107)								

positives: 88.8% identity: 88.8%

FIG. 21

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Section 1									
	1	10	20	30	40	53			
A15-3.45_HC	(1)	QVQLVQSGAEVKKKPGASVKVSCKASG	YTF	FSYGF	SWVRQAPGQGLEW	SGWISA			
VH1-18	(1)	QVQLVQSGAEVKKKPGASVKVSCKASG	YTF	TSYGF	SWVRQAPGQGLEW	SGWISA			
Consensus	(1)	QVQLVQSGAEVKKKPGASVKVSCKASG	YTF	SYG	SWVRQAPGQGLEW	SGWISA			
Section 2									
	54	60	70	80	90	106			
A15-3.45_HC	(54)	YNGNTNYAQKLQGRVTMTT	TD	STSTAYMELRSLRSD	DDTAVYYCAR	ETKVRGVH			
VH1-18	(54)	YNGNTNYAQKLQGRVTMTT	TD	STSTAYMELRSLRSD	DDTAVYYCAR	-----			
Consensus	(54)	YNGNTNYAQKLQGRVTMTT	TD	STSTAYMELRSLRSD	DDTAVYYCAR				
Section 3									
	107	123							
A15-3.45_HC	(107)	YYGMDVWGQGT	TVTVSS						
VH1-18	(99)	-----							
Consensus	(107)								

positives: 78.0% identity: 77.2%

FIG. 22

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Section 1						
	1	10	20	30	40	53
(1)	1					
A15-3.45_LC	(1)	DIYMTQSPDSLAVSLGERATI	IICKSSQSS	LYSSNNKNYL	GWYQQKPGQPPKLL	
B3	(1)	DIYMTQSPDSLAVSLGERATI	NCKSSQSS	LYSSNNKNYL	AWYQQKPGQPPKLL	
Consensus	(1)	DIYMTQSPDSLAVSLGERATI	CKSSQSS	LYSSNNKNYL	AWYQQKPGQPPKLL	
Section 2						
	54	60	70	80	90	106
(54)	54					
A15-3.45_LC	(54)	IYWASTRESGVPA	RFSGSGSGTDFLT	INSLQAED	VAVYCCQYYSTP	RSFGQ
B3	(54)	IYWASTRESGVPE	DRFSGSGSGTDFLT	INSLQAED	VAVYCCQYYSTP	-----
Consensus	(54)	IYWASTRESGVP	RFSGSGSGTDFLT	INSLQAED	VAVYCCQYYSTP	
Section 3						
	107	113				
(107)	107					
A15-3.45_LC	(107)	GTMVEIK				
B3	(102)	-----				
Consensus	(107)					

positives: 86.7%	identity: 85.0%
------------------	-----------------

FIG. 23

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Section 1									
(1)	1	10	20	30	40	53			
A15-3.65_HC	(1)	QVQLQESGPGLVKPSQTL	SLTCTVSGGS	INSGG	CYNSWIRQHPGKGL	EWI	GYI		
VH4-31	(1)	QVQLQESGPGLVKPSQTL	SLTCTVSGGS	INSGG	CYNSWIRQHPGKGL	EWI	GYI		
Consensus	(1)	QVQLQESGPGLVKPSQTL	SLTCTVSGGS	INSGG	CYNSWIRQHPGKGL	EWI	GYI		
Section 2									
(54)	54	60	70	80	90	106			
A15-3.65_HC	(54)	YS	SGSTYYNP	SLKSR	IN	SV	DT	SK	NQ
VH4-31	(54)	YS	SGSTYYNP	SLKSR	IN	SV	DT	SK	NQ
Consensus	(54)	YS	SGSTYYNP	SLKSR	IN	SV	DT	SK	NQ
Section 3									
(107)	107	119							
A15-3.65_HC	(107)	DYWGQG	TL	V	T	V	S	S	
VH4-31	(100)	-----							
Consensus	(107)	-----							

positives: 79.8% identity: 77.3%

FIG. 24

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		Section 1									
		1	10	20	30	40	50	60	70	80	90
(1)	1	DIQMTQSPSSLSASVGDRVTITTCQASQDI	NYLNWYQQKPGKAPKLLIYDASN								
A15-3.65_LC	(1)	DIQMTQSPSSLSASVGDRVTITTCQASQDI	NYLNWYQQKPGKAPKLLIYDASN								
O8	(1)	DIQMTQSPSSLSASVGDRVTITTCQASQDI	SNYLNWYQQKPGKAPKLLIYDASN								
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITTCQASQDI	NYLNWYQQKPGKAPKLLIYDASN								
		Section 2									
(54)	54	LETGVPSRFSGSGGTDFFTIS	GLQPEDIAITYCQQYD	TLPLTFGGG	TKVEI						
A15-3.65_LC	(54)	LETGVPSRFSGSGGTDFFTIS	GLQPEDIAITYCQQYD	TLPLTFGGG	TKVEI						
O8	(54)	LETGVPSRFSGSGGTDFFTIS	SLQPEDIAITYCQQYD	LP							
Consensus	(54)	LETGVPSRFSGSGGTDFFTIS	LQPEDIAITYCQQYD	LP							
		Section 3									
(107)	107										
A15-3.65_LC	(107)	K									
O8	(96)	-									
Consensus	(107)										

positives: 86.0%	identity: 86.0%
------------------	-----------------

FIG. 25

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		Section 1									
	(1)	1	10	20	30	40	53				
A15-6.1_HC	(1)	QVQLVESGGGVVQPG	SLRLSCAASGFTFS	SSYAMHWV	RQAPGK	GLEWVA	VISY				
VH3-30	(1)	QVQLVESGGGVVQPG	SLRLSCAASGFTFS	SSYAMHWV	RQAPGK	GLEWVA	VISY				
Consensus	(1)	QVQLVESGGGVVQPG	SLRLSCAASGFTFS	SSYAMHWV	RQAPGK	GLEWVA	VISY				
		Section 2									
	(54)	54	60	70	80	90	106				
A15-6.1_HC	(54)	DGSNKYYADSVKGRFTISRDNSKNTLYLQMN	SLRAEDTAVYYCAR	SIFGVVID							
VH3-30	(54)	DGSNKYYADSVKGRFTISRDNSKNTLYLQMN	SLRAEDTAVYYCAR	-----							
Consensus	(54)	DGSNKYYADSVKGRFTISRDNSKNTLYLQMN	SLRAEDTAVYYCAR	-----							
		Section 3									
	(107)	107	122								
A15-6.1_HC	(107)	YGMDVWGQGT	TVTVSS								
VH3-30	(99)	-----	-----								
Consensus	(107)	-----	-----								

positives: 80.3% identity: 79.5%

FIG. 26

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Section 1									
	1	10	20	30	40	54			
A15-6.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGT				RNYLAWYQQNPGKVPKLLIYGA	STL		
A20	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI				SNYLAWYQQKPGKVPKLLIYAA	STL		
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI				NYLAWYQQ	PGKVPKLLIYAA	STL	
Section 2									
	55	60	70	80	90	107			
A15-6.1_LC	(55)	QSGVPSRFSGSGGTDFTLTIS				SLOPEDVATYYCQKFS	SP	FTFGPGTKVDIS	
A20	(55)	QSGVPSRFSGSGGTDFTLTIS				SLOPEDVATYYCQKNN	SA	-----	
Consensus	(55)	QSGVPSRFSGSGGTDFTLTIS				SLOPEDVATYYCQKF	S	P	

positives: 85.0% identity: 83.2%

FIG. 27

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Section 1						
	(1)	1	10	20	30	53
A15-6.12_HC	(1)	QVQL	EQSGPGLVKPS	ETLSLTCTVSGGSISSG	TYHWSWIRQHPG	RGLEWIGYI
VH4-31	(1)	QVQL	QESGPGLVKPS	QTLSLTCTVSGGSISSG	GYHWSWIRQHPG	RGLEWIGYI
Consensus	(1)	QVQL	SGPGLVKPS	TLSLTCTVSGGSISSG	YHWSWIRQHPG	KGLEWIGYI
Section 2						
	(54)	54	60	70	80	106
A15-6.12_HC	(54)	YYSGSTYHNP	SLKSRNTISVDTSKNQFSLKLS	SVTAADTAVYYCAR	GGDGYR	
VH4-31	(54)	YYSGSTYHNP	SLKSRNTISVDTSKNQFSLKLS	SVTAADTAVYYCAR	-----	
Consensus	(54)	YYSGSTYHVP	SLKSRITISVDTSKNQFSLKLS	SVTAADTAVYYCAR		
Section 3						
	(107)	107	117			
A15-6.12_HC	(107)	WGQ	GLTVTVSS			
VH4-31	(100)	-----				
Consensus	(107)					

positives: 81.2%	identity: 77.8%
------------------	-----------------

FIG. 28

Section 1							
	(1)	1	10	20	30	40	53
L2	(1)	EIVMTQSPATLSVSPGERATLSCRASQSSNLLAWYQQKPGQAPRLINFGAST					
A15-6.12_LC	(1)	EIVMTQSPATLSVSPGERATLSCRASQSSNFAWYQQKPGQAPRLIIFGAST					
Consensus	(1)	EIVMTQSPATLSVSPGERATLSCRASQSSN AWYQQKPGQAPRLIIFGAST					
Section 2							
	(54)	54	60	70	80	90	106
L2	(54)	RATGIPAREFSGSGGTEFTLTISLSQSEDFAVYCCQYNNWP					---
A15-6.12_LC	(54)	RATGIPAREFSGSGGTEFTLTISLSQSEDFAVYCCQYNNWPERTFGQGTKVEI					---
Consensus	(54)	RATGIPAREFSGSGGTEFTLTISLSQSEDFAVYCCQYNNWP					
Section 3							
	(107)	107					
L2	(96)	-					
A15-6.12_LC	(107)	K					
Consensus	(107)						

positives: 86.9%	identity: 85.0%
------------------	-----------------

FIG. 29

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Section 1						
	(1)	1	10	20	30	53
A15-6.2_HC	(1)	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSTYYWSWIRQPPGKGLEWIGYIYY				
VH4-59	(1)	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSTYYWSWIRQPPGKGLEWIGYIYY				
Consensus	(1)	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSTYYWSWIRQPPGKGLEWIGYIYY				
Section 2						
	(54)	54	60	70	80	106
A15-6.2_HC	(54)	TGNITYNPISLKSRVTISVDTSKNQFSLKLNSVTTAADTAVYYCARDPGQWLVPD				
VH4-59	(54)	SGSTINYNPISLKSRVTISVDTSKNQFSLKLNSVTTAADTAVYYCAR				
Consensus	(54)	SG T YNPISLKSRVTISVDTSKNQFSLKL SVTTAADTAVYYCAR				
Section 3						
	(107)	107	121			
A15-6.2_HC	(107)	AFDIWGQGTMTVSVSS				
VH4-59	(98)	-----				
Consensus	(107)					

positives: 77.7%	identity: 75.2%
------------------	-----------------

FIG. 30

		Section 1									
		1	10	20	30	40	54				
A15-6.2_LC	(1)	DIVMTQSP LSLPV IPGEPAISCRSSQSLIQSNGNNYLDWYLQKPGQSPQILLIY									
A19	(1)	DIVMTQSP LSLPV IPGEPAISCRSSQSLIH SNGYNYLDWYLQKPGQSPQILLIY									
Consensus	(1)	DIVMTQSP LSLPV PGEPAISCRSSQSLI SNG NYLDWYLQKPGQSPQILLIY									
		Section 2									
		55	60	70	80	90	108				
A15-6.2_LC	(55)	LGSNRASGV PD RFSGSGGTDFTLKISRVEA EDVGN YYCMQALQIIPLTFGGGTK									
A19	(55)	LGSNRASGV PD RFSGSGGTDFTLKISRVEA EDVGN YYCMQALQITP-----									
Consensus	(55)	LGSNRASGV PD RFSGSGGTDFTLKISRVEADDVGIYYCMQALQ P									
		Section 3									
		(109)	109	112							
A15-6.2_LC	(109)	VEIK									
A19	(101)	----									
Consensus	(109)										

positives: 85.7%	identity: 83.9%
------------------	-----------------

FIG. 31

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		Section 1									
		1	10	20	30	40	53				
A15-6.9_HC	(1)	QVQL	EQSGPGLVKPS	ETLSLTCTVSGGSISSG	TYHNSWIRQHPG	RGLWIGYI					
VH4-31	(1)	QVQL	EQSGPGLVKPS	QTLSLTCTVSGGSISSG	YHNSWIRQHPG	RGLWIGYI					
Consensus	(1)	QVQL	SGPGLVKPS	TLSLTCTVSGGSISSG	YYWSWIRQHPG	KGLEWIGYI					
		Section 2									
		54	60	70	80	90	106				
A15-6.9_HC	(54)	YYSGSTYHNP	SLKSRNTISVDTSKNQFSLKLS	SVTAADTAVYYCAR	GGDG	YRY					
VH4-31	(54)	YYSGSTYHNP	SLKSRNTISVDTSKNQFSLKLS	SVTAADTAVYYCAR	GGDG	YRY					
Consensus	(54)	YYSGSTYHNP	SLKSRTISVDTSKNQFSLKLS	SVTAADTAVYYCAR							
		Section 3									
		(107)	107	117							
A15-6.9_HC	(107)	WGQGT	LVTVSS								
VH4-31	(100)	-----									
Consensus	(107)										

positives: 81.2%	identity: 77.8%
------------------	-----------------

FIG. 32

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		Section 1									
		1	10	20	30	40	54				
A15-6.9_LC	(1)	EIVMTQSPATLSVSPGERATLSCRASQSSNNFAWYQQKPGQAPRLIIFGASTR									
L2	(1)	EIVMTQSPATLSVSPGERATLSCRASQSSNNFAWYQQKPGQAPRLIIFGASTR									
Consensus	(1)	EIVMTQSPATLSVSPGERATLSCRASQSSNFAWYQQKPGQAPRLIIFGASTR									
		Section 2									
		55	60	70	80	90	107				
A15-6.9_LC	(55)	ATGIPARFSGSGGTEFTLTISLSQSEDFAVYYCQQYNNWPR						TFGQGTKVEIK			
L2	(55)	ATGIPARFSGSGGTEFTLTISLSQSEDFAVYYCQQYNNWPR						-----			
Consensus	(55)	ATGIPARFSGSGGTEFTLTISLSQSEDFAVYYCQQYNNWPR						-----			

positives: 86.9% identity: 85.0%

FIG. 33

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Section 1							
	(1)	1	10	20	30	40	53
A15-6.11_HC	(1)	QVQLQESGPGLVKPSQTL	SLTCTVSGGSISSG	THWTWIRQHPGKGLEWIGFI			
VH4-31	(1)	QVQLQESGPGLVKPSQTL	SLTCTVSGGSISSG	YHWSWIRQHPGKGLEWIGFI			
Consensus	(1)	QVQLQESGPGLVKPSQTL	SLTCTVSGGSISSG	YHWSWIRQHPGKGLEWIGFI			
Section 2							
	(54)	54	60	70	80	90	106
A15-6.11_HC	(54)	YYSGSTYYNP	SLKSRVTISVDTSKNQFSL	KLSSVTAADTAVYYCAR	GGDGYKY		
VH4-31	(54)	YYSGSTYYNP	SLKSRVTISVDTSKNQFSL	KLSSVTAADTAVYYCAR	GGDGYKY		
Consensus	(54)	YYSGSTYYNP	SLKSRVTISVDTSKNQFSL	KLSSVTAADTAVYYCAR	GGDGYKY		
Section 3							
	(107)	107	117				
A15-6.11_HC	(107)	WGQGT	LVTVSS				
VH4-31	(100)	-----					
Consensus	(107)	-----					

positives: 83.8%	identity: 82.9%
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FIG. 34

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Section 1		
	(1) 1	53
A15-6.11_LC	(1) EIVMTQSPATLSVSPGERATLSCRASQSVSNINLAWYQQKPGQAPRLIIYGAST	40
L2	(1) EIVMTQSPATLSVSPGERATLSCRASQSVSNINLAWYQQKPGQAPRLIIYGAST	30
Consensus	(1) EIVMTQSPATLSVSPGERATLSCRASQSVSNINLAWYQQKPGQAPRLIIYGAST	20
Section 2		
	(54) 54	106
A15-6.11_LC	(54) RATGIPARFSGSGGTEFTLTISSLQSEDFAVYICQQYNNWPRTFGQGTKVEI	90
L2	(54) RATGIPARFSGSGGTEFTLTISSLQSEDFAVYICQQYNNWPRTFGQGTKVEI	80
Consensus	(54) RATGIPARFSGSGGTEFTLTISSLQSEDFAVYICQQYNNWPRTFGQGTKVEI	70
Section 3		
	(107) 107	
A15-6.11_LC	(107) K	
L2	(96) -	
Consensus	(107)	

positives: 87.9% identity: 87.9%

FIG. 35

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Clone #	VH	#del	VH End	#N's	N Sequence	DH	Size of D	D Sequence	#N's	N Sequence	JH	#del	JH Segment
A15-3.10	DP-71/4-59	0	GAGAGA	8	TCAGGGGC	D21-9	8	AGTGGTTA	7	CTACCCG	JH3B	0	ATGCTT
A15-3.22	DP-65/4-31	0	GAGAGA	9	GGGAGATGG	-	-	-	-	-	JH4B	-4	CTTTGA
A15-3.27	DP-71/4-59	0	GAGAGA	8	TCAGGGGC	D21-9	8	AGTGGTTA	7	CTACCCG	JH3B	0	ATGCTT
A15-3.45	DP-14/1-18	0	GAGAGA	6	AACTAA	D3-10	12	GGTTCGGGAGT	2	CC	JH6B	-9	ACTACT
A15-3.65	DP-65/4-31	0	GAGAGA	8	TCGGGAAA	D6-13	8	CAGCTGGT	4	TTTT	JH5A	-11	GA CTAC
A15-6.1	DP-49/3-30	3	GAGAGA	1	T	D3-3	18	CGATTTTGGAGTGGTTA	3	TCG	JH6B	-12	ACTACG
A15-6.2	DP-71/4-59	0	GAGAGA	7	TCCAGGC	D6-19	11	CAGTGGCTGGT	5	CCTG	JH3B	0	ATGCTT
A15-6.9	DP-65/4-31	1	CGAGAG	3	GGG	D5-24	11	GAGATGGCTAC	4	AGAT	JH1	-16	ACTGGG
A15-6.11	DP-65/4-31	1	CGAGAG	3	GGG	D5-24	13	GAGATGGCTACAA	2	GT	JH1	-16	ACTGGG
A15-6.12	DP-65/4-31	1	CGAGAG	3	GGG	D5-24	11	GAGATGGCTAC	4	AGAT	JH1	-16	ACTGGG

Clone #	VK	#del	VH End	#N's	N Sequence	JK	#del	JK end
A15-3.10	02/012/DPK	0	CCCTCC	9	GGAGTGCAG	JK2	-7	TTTTGG
A15-3.22	A30	3	TTACCC	0	0	JK4	0	GCTCAC
A15-3.27	A30	3	TTACCC	0	0	JK1	0	GTGGAC
A15-3.45	B3/DPK24	1	TCCCTC	3	GGT	JK1	-5	CGTTCG
A15-3.65	08/018/DPK	1	TCCCTC	0	0	JK4	-2	TCAC TTTC
A15-6.1	A20/DPK4	3	GTCCCC	0	0	JK3	0	ATTCAC
A15-6.2	A3/A19/DPK	1	TTCCTC	0	0	JK4	-2	TCAC TTTC
A15-6.9	L2/DPK21	1	GGCCTC	0	0	JK1	-2	GGACGTT
A15-6.11	L2/DPK21	1	GGCCTC	0	0	JK1	-2	GGACGTT
A15-6.12	L2/DPK21	1	GGCCTC	0	0	JK1	-2	GGACGTT

FIG. 36